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### **Microbial communities: temporal and biogeographic structure**

Coming primarily from a marine background I have been very interested in how bacteria exist in such a fluid matrix. Specifically, what determines how microbes exist when the medium in which they live is moving around so much? My research site in the Western English Channel has demonstrated that even though the sampling location is flushed with new water every two weeks, the same communities of microbes appear year after year. This highlights that microbes exist in robust and well-defined communities in this ecosystem. My ongoing research is to determine how true this is for all ecosystems around the planet.

### **Taxonomic diversity**

There are a nonillion bacteria in the world ( $1 \times 10^{30}$  cells) give or take a few quadrillion. This almost incomprehensible number is greater than the number of stars in the known universe. To date no one has ever fully characterized the biodiversity of a microbial sample. Even the simplest communities seem to have a never-ending 'tail' of rare microorganisms, some of which seem to respond to episodic events producing 'blooms', while others seem to just exist in this rare state. We have now applied more than 20 million sequences to one sample from a marine ecosystem and still failed to catalogue all the diversity therein. Until we are able to fully characterize one of these communities, every effort to describe the global extent of microbial diversity will be extrapolative. Understanding biodiversity in any ecosystem, gives you an appropriate metric by which to describe it. Until we can do that we are describing the relative abundance of a subset of a given community. Understanding this concept, and exploring the limits of diversity are fundamental to my research goals.

### **Microbial Metabolic Dynamics**

Microbes are vital to the success of life on this planet. They perform the vast majority of all metabolic processes, and also control health in every living organism on this planet. My lab uses metagenomics (literally meaning 'beyond the genome') to characterize the metabolic potential of a microbial community. We also use metatranscriptomics to explore the genes that are transcribed in every cell in a community. We then turn the sequence data into metabolic information by ascribing function to each potential gene or transcript and then defining their metabolic activity. Through comparison between one sample and another we can effectively describe how the metabolic activity of a community changes over time or space. This is essential to exploring functional and trophic interactions in a community, i.e. who eats who, who feeds on what, and who needs what?

## Recent publications:

### 2011

1. Temperton B, Thomas S, Tait K, Parry H, Emery M, Allen M, Quinn J, McGrath J, **Gilbert JA**. 2011. Permanent draft genome sequence of *Vibrio tubiashii* strain NCIMB 1337 (ATCC19106). SIGS. *In press*.
2. Field D, Kyrpides N, White O, Knight R, **Gilbert JA**, et al. 2011. The Genomic Standards Consortium, Plos Biology. *In press*.
3. Best A, DeJongh M, DevoidS, **Gilbert JA**, Glass E, Henry CS, Larsen P, Meyer F, Overbeek R, Stevens RL, Vonstein V, Wilke A, Wilkening J, Xia F. 2011. Predicting Phenotype from Genotype with SEED. Biochimica et Biophysica Acta General Subjects. *In Press*.
4. Laverock B, **Gilbert JA**, Tait K, Osborn AM, Widdicombe S. 2011. Bioturbation: impact on the marine nitrogen cycle. Biochem Soc Trans. 39(1):315-20.
5. Yilmaz P, **Gilbert JA**, Knight R, Amaral-Zettler L, Mizrachi I, Chochrane G, Nakamura Y, Assunta-Sansone S, Glockner F-O, Field D. 2011. The Genomic Standards Consortium: Bringing Standards to Life for Microbial Ecology. ISME J. *In press*.
6. Yilmaz P, Kottmann R, Field D, Knight R, Cole JR, Amaral-Zettler L, **Gilbert JA** et al. 2011. The "Minimum Information about an ENvironmental Sequence" (MIENS) specification. Nature Biotechnology. *In press*.
7. Cooley NA, Kulakova AN, Villareal-Chiu JF, **Gilbert JA**, McGrath JW, Quinn JP. 2011. Phosphonoacetate biosynthesis: *In vitro* detection of a novel NADP<sup>+</sup>-dependent phosphonoacetaldehyde-oxidizing activity in cell-extracts of a marine *Roseobacter*. Mikrobiology. *In press*.
8. Turk K, Pereira N, Swift P, Shelley R, Zehr J, Lohan M, Woodward EMS, Rees A, **Gilbert JA**. 2011. Nitrogen fixation across a gradient of primary productivity. ISME J. doi:10.1038/ismej.2010.205
9. **Gilbert JA**, Meyer F and Bailey M. 2011. The Future of microbial metagenomics (or is ignorance bliss?). ISME J. 5, 777-779.
10. **Gilbert JA** and Dupont C. 2011. Marine Metagenomics. Annual Review of Marine Science. Volume 3: 347-371.
11. Larsen PE, Collart F, Field D, McGrath J, Quinn J, **Gilbert JA**. 2011. Predicted Relative Metabolomic Turnover (PRMT): determining metabolic turnover from a coastal marine metagenomic dataset. Conference proceedings for BIOSTEC 2011; Meta2011, Metagenomic Sequence Data Analysis. January 28<sup>th</sup>-29<sup>th</sup>, 2011.
12. Temperton B, **Gilbert JA**, Quinn JP, McGrath JW. 2011. Novel Analysis of Oceanic Surface Water Metagenomes Suggests Importance of Polyphosphate Metabolism in Oligotrophic Environments. PLoS ONE 6(1): e16499. doi:10.1371/journal.pone.0016499
13. **Gilbert JA**, O'Dor R, Vogel T. 2011. Survey studies are still vital to science. Nature. 469, 162.
14. **Gilbert J.A.**, Laverock B, Temperton B, Thomas S, Mühling M and Hughes M. 2011. Metagenomic protocols. 2011. In: Methods in Molecular Biology, Vol 733: *High-throughput Sequencing: Applications to Microbiology*. Kwon, Young Min; Ricke, Steven C. (Eds.) Springer. ISBN: 978-1-61779-088-1.
15. **Gilbert J.A.** and Hughes M. 2011. Gene Expression Profiling: Metatranscriptomics. In: Methods in Molecular Biology, Vol 733: *High-throughput Sequencing: Applications to Microbiology*. Kwon, Young Min; Ricke, Steven C. (Eds.) Springer. ISBN: 978-1-61779-088-1.

### 2010

16. **Gilbert JA**, Meyer F, Knight R, Field D, Kyrpides N, Yilmaz P, Wooley J. 2010. Meeting report: GSC M5 roundtable at the 13<sup>th</sup> International Society for Microbial Ecology meeting in Seattle, WA, USA, August 22-27<sup>th</sup> 2010. Standards in Genomic Science. 3:3
17. **Gilbert JA**, Meyer F, Antonopoulos D, Balaji P, Brown CT, Brown CT, Desai N, Eisen JA, Evers D, Feng W, Huson D, Jasson J, Knight R, Knight J, Kolker E, Kostantindis K, Kostka J, Kyrpides, N, Mackelprang R, McHardy A, Quince C, Raes J, Sczyrba A, Shade A, Stevens R. 2010. Meeting Report. The Terabase Metagenomics Workshop and the Vision of an Earth Microbiome Project.

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18. **Gilbert JA**, Meyer F, Jansson J, Gordon J, Pace N, Tiedje J, Ley R, Fierer N, Field D, Kyrpides N, Glockner F-O, Klenk H-P, Wommack KE, Glass E, Docherty K, Gallery R, Stevens R, Knight R. 2010. The Earth Microbiome Project: Meeting report of the “1<sup>st</sup> EMP meeting on sample selection and acquisition” at Argonne National Laboratory October 6<sup>th</sup> 2010. Standards in Genomic Science. 3:3.
  19. Glass E, Meyer F, **Gilbert JA**, Field D, Hunter S, Kottman R, Kyrpides N, Sansone S, Schriml L, Sterk P, White O, Wooley J. 2010. Meeting report from the Genomics Satndards Consortium (GSC) workshop 10. SIGS 3:3.
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  22. Mitra S, Rupek P, Urich T, **Gilbert JA**, Meyer F, Huson DH. 2010. Functional analysis of meta-genomes and –transcriptomes using SEED and KEGG. BMC Bioinformatics. 12(Suppl 1):S12+.
  23. **Gilbert JA**, Meyer F, Joint I, Mühling M, Field D. 2010. Short Metagenome Report: Metagenomes and metatranscriptomes from the L4 long term coastal monitoring station in the Western English Channel. SIGS. Vol 3 (2).
  24. **Gilbert JA**, Meyer F, Field D, Schriml LM, Garrity GM. 2010. Metagenomics: A foundling finds its feet. SIGS. Vol 3 (2).
  25. Heidelberg KB, **Gilbert JA** and Joint I. 2010. Mini Review: Marine genomics: at the interface of marine microbial ecology and biodiscovery. Microbial Biotechnology. 3(5), 531–543
  26. Laverock B., Widdicombe S, Tait K, Smith C, Osborn M, **Gilbert JA**. 2010. The impact of burrowing shrimp on bacterial diversity in temperate coastal sediments. ISME J. 4, 1531–1544.
  27. Hirschman L., Sterk P., Field D., Wooley J., Cochrane G., **Gilbert JA.**, Kolker E., Kyrpides N., Meyer F., Mizrahi I., Nakamura Y., Sansone S., Schriml L., Tatusova T., White O. and Yilmaz P. 2010. Meeting Report: “Metagenomics, Metadata and Meta-analysis” (M3) Workshop at the Pacific Symposium on Biocomputing 2010. Standards in Genomic Sciences, Vol 2, No 3
  28. **Gilbert JA**. 2010. Beyond the Infinite – tracking bacterial gene expression. Microbiology Today. 37:2; 82-85.
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  33. Thomas S, Burdett H, Temperton B, Wick R, Snelling D, Woodward M, McGrath J, Quinn J, Munn C and **Gilbert JA**. 2010. The diversity of *phnA* gene homologues in temperature-stressed Cnidarian-associated Bacteria. ISME J. doi:10.1038/ismej.2009.129

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34. **Gilbert JA**, Field D, Swift P, Newbold L, Oliver A, Smyth T, Somerfield P, Huse S, Joint I. 2009. Seasonal succession of microbial communities in the Western English Channel using 16S rDNA-tag pyrosequencing. Env. Microb. 11(12), 3132–3139
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40. Rees AP, **Gilbert JA**, Kelly-Gerrey BA. 2008. Evidence of Nitrogen fixation in a temperate coastal sea (western English Channel). *MEPS.* Vol. 374: 7–12
41. **Gilbert JA**, Field D, Huang Y, Edwards R, Li W, et al. (2008) Detection of Large Numbers of Novel Sequences in the Metatranscriptomes of Complex Marine Microbial Communities. *PLoS ONE* 3(8): e3042. doi:10.1371/journal.pone.0003042
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43. Susanna-Assunta Sansone, Philippe Rocca-Serra, Dawn Field, **Jack Gilbert**, et al. 2008. The first RSBI (ISA-TAB) workshop: “can a simple format work for complex studies?”. *OMICS.* 12(2):143-9.
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45. Garnham C.P.<sup>†</sup>, **Gilbert JA**<sup>\*</sup>, Hartman C<sup>†</sup>, Campbell RL<sup>†</sup>, Laybourn-Parry J.<sup>‡</sup> and Davies PL. 2008. Ca<sup>2+</sup>-dependent bacterial antifreeze protein domain has a novel beta-helical ice-binding fold. *Biochem J.* 2007 Dec 20; [Epub ahead of print].

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48. **Gilbert, J. A.**; Davies, P.L.; Laybourn-Parry, J. (2005). A hyperactive, Ca<sup>2+</sup>-dependent antifreeze protein in an Antarctic bacterium. *FEMS Microbiology Letters.* 245(1), 67-72.

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50. Tomczak, M. M.; Marshall, C. B.; **Gilbert, J. A.** and Davies, P. L. (2003). A facile method for determining ice recrystallisation inhibition by antifreeze proteins. *Biochemical and Biophysical*

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